



IFWO

RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/695,568

TIME: 12:54:54

Input Set : N:\Cr3\RULE60\10695568.raw

Output Set: N:\CRF4\08302004\J695568.raw

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1 <110> APPLICANT: Elizabeth J. Ackermann
2      C. Frank Bennett
3      Hong Zhang
4      Andrew T. Watt
5      William Ricketts
6      Nicholas M. Dean
7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF FLIP-C EXPRESSION
8 <130> FILE REFERENCE: RTS-0202
9 <140> CURRENT APPLICATION NUMBER: US/10/695,568
10 <141> CURRENT FILING DATE: 2003-10-27
11 <150> PRIOR APPLICATION NUMBER: US/09/666,269
12 <151> PRIOR FILING DATE: 2000-09-20
13 <160> NUMBER OF SEQ ID NOS: 133
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 20
16 <212> TYPE: DNA
17 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: Antisense Oligonucleotide
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23 <210> SEQ ID NO: 2
24 <211> LENGTH: 20
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Antisense Oligonucleotide
29 <400> SEQUENCE: 2
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33 <211> LENGTH: 2770
34 <212> TYPE: DNA
35 <213> ORGANISM: Mus musculus
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (75)...(1529)
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41      ctgtggttct gaac atg gcc cag agc cct gtg tct gcc gag gtc att cac      110
42                  Met Ala Gln Ser Pro Val Ser Ala Glu Val Ile His
43                  1              5              10
44      cag gtg gaa gag tgt ctt gat gaa gac gag aag gag atg atg ctc ttc      158
45      Gln Val Glu Glu Cys Leu Asp Glu Asp Glu Lys Glu Met Met Leu Phe

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ENTERED

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46	15				20				25								
47	ctg	tgt	aga	gat	gtg	act	gag	aac	ctg	gct	gca	cct	aac	gtc	agg	gac	206
48	Leu	Cys	Arg	Asp	Val	Thr	Glu	Asn	Leu	Ala	Ala	Pro	Asn	Val	Arg	Asp	
49	30				35				40								
50	ctc	ctg	gat	agc	tta	agt	gag	aga	ggc	cag	ctc	tct	ttt	gct	acc	ttg	254
51	Leu	Leu	Asp	Ser	Leu	Ser	Glu	Arg	Gly	Gln	Leu	Ser	Phe	Ala	Thr	Leu	
52	45				50				55				60				
53	gct	gaa	ttg	ctc	tac	aga	gtg	agg	cgg	ttt	gac	ctt	ctc	aag	agg	atc	302
54	Ala	Glu	Leu	Leu	Tyr	Arg	Val	Arg	Arg	Phe	Asp	Leu	Leu	Lys	Arg	Ile	
55	65				70				75								
56	ttg	aag	aca	gac	aaa	gca	acc	gtg	gag	gac	cac	ctg	cgc	aga	aac	cct	350
57	Leu	Lys	Thr	Asp	Lys	Ala	Thr	Val	Glu	Asp	His	Leu	Arg	Arg	Asn	Pro	
58	80				85				90								
59	cac	ctg	gtt	tct	gat	tat	agg	gtc	ctg	ctg	atg	gag	att	ggg	gag	agc	398
60	His	Leu	Val	Ser	Asp	Tyr	Arg	Val	Leu	Leu	Met	Glu	Ile	Gly	Glu	Ser	
61	95				100				105								
62	tta	gat	cag	aac	gat	gta	tcc	tcc	tta	gtt	ttc	ctt	aca	agg	att	aca	446
63	Leu	Asp	Gln	Asn	Asp	Val	Ser	Ser	Leu	Val	Phe	Leu	Thr	Arg	Ile	Thr	
64	110				115				120								
65	agg	gat	tac	aca	ggc	aga	ggc	aag	ata	gcc	aag	gac	aag	agt	ttc	ttg	494
66	Arg	Asp	Tyr	Thr	Gly	Arg	Gly	Lys	Ile	Ala	Lys	Asp	Lys	Ser	Phe	Leu	
67	125				130				135				140				
68	gat	ctg	gtg	att	gaa	ttg	gag	aaa	ctg	aat	cta	att	gct	tca	gac	caa	542
69	Asp	Leu	Val	Ile	Glu	Leu	Glu	Lys	Leu	Asn	Leu	Ile	Ala	Ser	Asp	Gln	
70	145				150				155								
71	ttg	aat	ttg	tta	gaa	aaa	tgc	ctg	aag	aac	atc	cac	aga	ata	gac	ttg	590
72	Leu	Asn	Leu	Leu	Glu	Lys	Cys	Leu	Lys	Asn	Ile	His	Arg	Ile	Asp	Leu	
73	160				165				170								
74	aac	aca	aag	atc	cag	aag	tac	acc	cag	tcc	agc	caa	gga	gca	aga	tca	638
75	Asn	Thr	Lys	Ile	Gln	Lys	Tyr	Thr	Gln	Ser	Ser	Gln	Gly	Ala	Arg	Ser	
76	175				180				185								
77	aat	atg	aat	act	ctc	cag	gct	tcg	ctc	cca	aaa	ttg	agt	atc	aag	tat	686
78	Asn	Met	Asn	Thr	Leu	Gln	Ala	Ser	Leu	Pro	Lys	Leu	Ser	Ile	Lys	Tyr	
79	190				195				200								
80	aac	tca	agg	ctc	cag	aat	ggg	cga	agt	aaa	gag	cca	aga	ttt	gtg	gaa	734
81	Asn	Ser	Arg	Leu	Gln	Asn	Gly	Arg	Ser	Lys	Glu	Pro	Arg	Phe	Val	Glu	
82	205				210				215				220				
83	tac	cgt	gac	agt	caa	aga	aca	ctg	gtg	aag	aca	tcc	atc	cag	gaa	tca	782
84	Tyr	Arg	Asp	Ser	Gln	Arg	Thr	Leu	Val	Lys	Thr	Ser	Ile	Gln	Glu	Ser	
85	225				230				235								
86	gga	gct	ttt	tta	cct	ccg	cac	atc	cgt	gaa	gag	act	tac	agg	atg	cag	830
87	Gly	Ala															

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Input Set : N:\CrF3\RULE60\10695568.raw

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95      ctt ttc ttg ttt ccc aag tca cat gac ata acc cag att gtt cgc cga      974
96      Leu Phe Leu Phe Pro Lys Ser His Asp Ile Thr Gln Ile Val Arg Arg
97      285                290                295                300
98      tat gca agt atg gcc caa cat caa gac tat gac agc ttt gca tgt gtt      1022
99      Tyr Ala Ser Met Ala Gln His Gln Asp Tyr Asp Ser Phe Ala Cys Val
100             305                310                315
101      ctg gtg agc cta gga ggc tcc caa agc atg atg ggc aga gat caa gtt      1070
102      Leu Val Ser Leu Gly Gly Ser Gln Ser Met Met Gly Arg Asp Gln Val
103             320                325                330
104      cac tca ggg ttc tcc ttg gat cat gtc aag aac atg ttc acg ggg gac      1118
105      His Ser Gly Phe Ser Leu Asp His Val Lys Asn Met Phe Thr Gly Asp
106             335                340                345
107      acg tgc cct tct ctc aga ggg aag cca aag ctc ttt ttt att cag aac      1166
108      Thr Cys Pro Ser Leu Arg Gly Lys Pro Lys Leu Phe Phe Ile Gln Asn
109             350                355                360
110      tat gag tcg tta ggt agc cag ttg gaa gat agc agc ctg gag gta gat      1214
111      Tyr Glu Ser Leu Gly Ser Gln Leu Glu Asp Ser Ser Leu Glu Val Asp
112      365                370                375                380
113      ggg cca tca ata aaa aat gtg gac tct aag ccc ctg caa ccc aga cac      1262
114      Gly Pro Ser Ile Lys Asn Val Asp Ser Lys Pro Leu Gln Pro Arg His
115             385                390                395
116      tgc aca act cac cca gaa gct gat atc ttt tgg agc ctg tgc aca gca      1310
117      Cys Thr Thr His Pro Glu Ala Asp Ile Phe Trp Ser Leu Cys Thr Ala
118             400                405                410
119      gac gta tct cac ttg gag aag ccc tcc agc tca tcc tct gtg tat ctg      1358
120      Asp Val Ser His Leu Glu Lys Pro Ser Ser Ser Ser Ser Val Tyr Leu
121             415                420                425
122      cag aag ctc tcc cag cag ctg aag caa ggc agg aga cgc cca ctc gtg      1406
123      Gln Lys Leu Ser Gln Gln Leu Lys Gln Gly Arg Arg Arg Pro Leu Val
124             430                435                440
125      gac ctc cac gtt gaa ctc atg gac aaa gtg tat gcg tgg aac agt ggt      1454
126      Asp Leu His Val Glu Leu Met Asp Lys Val Tyr Ala Trp Asn Ser Gly
127      445                450                455                460
128      gtt tcg tct aag gag aaa tac agc ctc agc ctg cag cac act ctg agg      1502
129      Val Ser Ser Lys Glu Lys Tyr Ser Leu Ser Leu Gln His Thr Leu Arg
130             465                470                475
131      aag aaa ctc atc ctg gct cct acg tga gaacccacaga ccgttggtgt      1549
132      Lys Lys Leu Ile Leu Ala Pro Thr
133      480                485
134      tcttggtata tcatccaggg tggcggcttg gagcagagct tggcgggttac ggctgcttct      1609
135      ggctgcttct ggctctgccg tgagtcctgg cctagggttc tcctgtgcac aggcattgagc      1669
136      cgtaaccctg tgcctgggaa acgtctcact ccgcgcgcg tgcctttacc tctctaaact      1729
137      tccctactta cattccttag tcggatgttt tgccagagtg tggagaacag taagacataa      1789
138      acctattgtt tgtttgtttt tttggggggg aggttatcta ccaagttata ccaagttatt      1849
139      gtatgggtgt atagtgtata gtggttcaag attctgaatg taacttgaga cttacctgag      1909
140      tttgtcatgc gactgggtaa attgtttcta tggcacatct aatcatttaa taagtaatta      1969
141      cctcattaag taccattgc ttcaggactt tcacattggc caccaatttc tgtgaccag      2029
142      ctccacattt atattctctt tcggcaaaac caaatttcat tatgtctgtt taatatctac      2089
143      agtctaattgc tttgtaagac atctagatag gaaaaatagt taccattgag cacaggagg      2149

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144      ctggcctgac cctcaccagc tgtgcagtgg cttcggtgaa aggagaaatga gccctactcc 2209
145      ttgaaagggt gtagtgcttg ggagagcagt ctgtaccttg cctgggcagc acagtagagc 2269
146      cagccccaag aacacaacag tgagtggggg agcttgccct ggttggctca ggatcaggaa 2329
147      acaggagggg tgaccaactt ggggctttga ggtggccac cccagcatcc atatcatctg 2389
148      tgaactgcca gagcctgtga aggggagggt cctgtagaac taaggctgca ggatctccat 2449
149      gacacagggc aacaacaggg tatctgagaa ggggtcccggt gaggggtccag tatttatagt 2509
150      gcaccagaag ccagaggcct cggatcagac aatgacccat tgcactgagt aaagatgtaa 2569
151      gtgaatgagt gaagatgtgt gggcacacgg aaatactgag ggacacacac aagcttttat 2629
152      ggagatgttt gtttgtttgt ttgtttgttt tttgtttctt tggcaggaac agattgcaag 2689
153      ggcagagagt agataaggaa gctggagaca tgagtggggg tgggtgcatg atatagaatt 2749
154      cacaaagaaa aaaaaaaaaa a                                     2770
156 <210> SEQ ID NO: 4
157 <211> LENGTH: 20
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: PCR Primer
162 <400> SEQUENCE: 4
163      gagaaccca gaccgttggt                                     20
165 <210> SEQ ID NO: 5
166 <211> LENGTH: 18
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: PCR Primer
171 <400> SEQUENCE: 5
172      agccgtaacc gccaaagt                                     18
174 <210> SEQ ID NO: 6
175 <211> LENGTH: 23
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: PCR Probe
180 <400> SEQUENCE: 6
181      ccaagccgcc accctggatg ata                                     23
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 20
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: PCR Primer
189 <400> SEQUENCE: 7
190      ggcaaatcca acggcacagt                                     20
192 <210> SEQ ID NO: 8
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: PCR Primer

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199 gggctctcgct cctggaagct 20
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202 <211> LENGTH: 27
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: PCR Probe
207 <400> SEQUENCE: 9
208 aaggccgaga atgggaagct tgtcatc 27
210 <210> SEQ ID NO: 10
211 <211> LENGTH: 1062
212 <212> TYPE: DNA
213 <213> ORGANISM: Homo sapiens
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (294)...(959)
217 <400> SEQUENCE: 10
218 gcacgagcgg cacgagtaga cttctataga tccctttcta tagaacttaa tctacttaag 60
219 tcaggagac caccagaag gaaagagccc atactttcaa tcttaggcat aagttagctt 120
220 gataagattt tcagaaaaat tcccttttaa ccacagaact cccccactgg aaaggattct 180
221 gaaagaaatg aagtcagccc tcagaaatga agttgactgc ctgctggctt tctgttgact 240
222 ggcccgagc tgtactgcaa gacccttgag agcttcctta gtctaagagt agg atg 296
223 Met
224 1
225 tct gct gaa gtc atc cat cag gtt gaa gaa gca ctt gat aca gat gag 344
226 Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp Glu
227 5 10 15
228 aag gag atg ctg ctc ttt ttg tgc cgg gat gtt gct ata gat gtg gtt 392
229 Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val Val
230 20 25 30
231 cca cct aat gtc agg gac ctt ctg gat att tta cgg gaa aga ggt aag 440
232 Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly Lys
233 35 40 45
234 ctg tct gtc ggg gac ttg gct gaa ctg ctc tac aga gtg agg cga ttt 488
235 Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg Phe
236 50 55 60 65
237 gac ctg ctc aaa cgt atc ttg aag atg gac aga aaa gct gtg gag acc 536
238 Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu Thr
239 70 75 80
240 cac ctg ctc agg aac cct cac ctt gtt tcg gac tat aga gtg ctg atg 584
241 His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met
242 85 90 95
243 gca gag att ggt gag gat ttg gat aaa tct gat gtg tcc tca tta att 632
244 Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu Ile
245 100 105 110
246 ttc ctc atg aag gat tac atg ggc cga ggc aag ata agc aag gag aag 680
247 Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys
248 115 120 125

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:22; N Pos. 521

Seq#:133; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10695568.raw

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L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:480
L:1661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:0